

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=20; hr=11; min=45; sec=45; ms=947;
]

=====

Application No: 10578615 Version No: 1.0

Input Set:**Output Set:**

Started: 2007-12-20 11:22:49.812
Finished: 2007-12-20 11:22:51.814
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 2 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-12-20 11:22:49.812
Finished: 2007-12-20 11:22:51.814
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 2 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)

SEQUENCE LISTING

<110> Tohata, Masatoshi
Sawada, Kazuhisa
Ozaki, Katsuya
Sekiguchi, Junichi

<120> RECOMBINANT MICROORGANISM

<130> 288704US0PCT

<140> 10578615

<141> 2007-12-20

<150> PCT/JP04/16890

<151> 2004-11-05

<150> JP 2003-379114

<151> 2003-11-07

<160> 22

<170> PatentIn version 3.3

<210> 1

<211> 3150

<212> DNA

<213> Bacillus sp. KSM-S237

<220>

<221> CDS

<222> (573)..(3044)

<220>

<221> sig_peptide

<222> (573)..(659)

<400> 1

gatttgccga tgcaacaggc ttatatattag aggaaatttc tttttaaatt gaatacggaa	60
taaaatcagg taaacaggtc ctgattttat ttttttgagt ttttagaga actgaagatt	120
gaaataaaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac	180
gcctttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata	240
aaaccttata ttccggctct tttttaaaac agggggtaaa aattcactct agtattctaa	300
tttcaacatg ctataataaa ttgtgaagac gcaatatgca tctctttttt tacgatatat	360
gtaagcgggtt aaccttgtgc tatatgccga ttttaggaagg ggggtagatt gagtcaagta	420
gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca	480
agttttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga	540

ttcaattact ttaaaaatat ttaggaggta at atg atg tta aga aag aaa aca	593
Met Met Leu Arg Lys Lys Thr	
1 5	
aag cag ttg att tct tcc att ctt att tta gtt tta ctt cta tct tta	641
Lys Gln Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Leu Ser Leu	
10 15 20	
ttt ccg gca gct ctt gca gca gaa gga aac act cgt gaa gac aat ttt	689
Phe Pro Ala Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe	
25 30 35	
aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc	737
Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly	
40 45 50 55	
gca tta caa tta caa gaa gtc gat gga caa atg aca tta gta gat caa	785
Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln	
60 65 70	
cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag	833
His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln	
75 80 85	
tgg ttt cct gag atc ttg aat gat aac gca tac aaa gct ctt tct aac	881
Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn	
90 95 100	
gat tgg gat tcc aat atg att cgt ctt gct atg tat gta ggt gaa aat	929
Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn	
105 110 115	
ggg tac gct aca aac cct gag tta atc aaa caa aga gtg att gat gga	977
Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gln Arg Val Ile Asp Gly	
120 125 130 135	
att gag tta gcg att gaa aat gac atg tat gtt att gtt gac tgg cat	1025
Ile Glu Leu Ala Ile Glu Asn Asp Met Tyr Val Ile Val Asp Trp His	
140 145 150	
gtt cat gcg cca ggt gat cct aga gat cct gtt tat gca ggt gct aaa	1073
Val His Ala Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys	
155 160 165	
gat ttc ttt aga gaa att gca gct tta tac cct aat aat cca cac att	1121
Asp Phe Phe Arg Glu Ile Ala Ala Leu Tyr Pro Asn Asn Pro His Ile	
170 175 180	
att tat gag tta gcg aat gag ccg agt agt aat aat aat ggt gga gca	1169
Ile Tyr Glu Leu Ala Asn Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala	
185 190 195	
ggg att ccg aat aac gaa gaa ggt tgg aaa gcg gta aaa gaa tat gct	1217
Gly Ile Pro Asn Asn Glu Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala	
200 205 210 215	

gat cca att gta gaa atg tta cgt aaa agc ggt aat gca gat gac aac	1265
Asp Pro Ile Val Glu Met Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn	
220 225 230	
att atc att gtt ggt agt cca aac tgg agt cag cgt ccg gac tta gca	1313
Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala	
235 240 245	
gct gat aat cca att gat gat cac cat aca atg tat act gtt cac ttc	1361
Ala Asp Asn Pro Ile Asp Asp His His Thr Met Tyr Thr Val His Phe	
250 255 260	
tac act ggt tca cat gct gct tca act gaa agc tat ccg tct gaa act	1409
Tyr Thr Gly Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr	
265 270 275	
cct aac tct gaa aga gga aac gta atg agt aac act cgt tat gcg tta	1457
Pro Asn Ser Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu	
280 285 290 295	
gaa aac gga gta gcg gta ttt gca aca gag tgg gga acg agt caa gct	1505
Glu Asn Gly Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala	
300 305 310	
agt gga gac ggt ggt cct tac ttt gat gaa gca gat gta tgg att gaa	1553
Ser Gly Asp Gly Gly Pro Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu	
315 320 325	
ttt tta aat gaa aac aac att agc tgg gct aac tgg tct tta acg aat	1601
Phe Leu Asn Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn	
330 335 340	
aaa aat gaa gta tct ggt gca ttt aca cca ttc gag tta ggt aag tct	1649
Lys Asn Glu Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser	
345 350 355	
aac gca acc aat ctt gac cca ggt cca gat cat gtg tgg gca cca gaa	1697
Asn Ala Thr Asn Leu Asp Pro Gly Pro Asp His Val Trp Ala Pro Glu	
360 365 370 375	
gaa tta agt ctt tct gga gaa tat gta cgt gct cgt att aaa ggt gtg	1745
Glu Leu Ser Leu Ser Gly Glu Tyr Val Arg Ala Arg Ile Lys Gly Val	
380 385 390	
aac tat gag cca atc gac cgt aca aaa tac acg aaa gta ctt tgg gac	1793
Asn Tyr Glu Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp	
395 400 405	
ttt aat gat gga acg aag caa gga ttt gga gtg aat tcg gat tct cca	1841
Phe Asn Asp Gly Thr Lys Gln Gly Phe Gly Val Asn Ser Asp Ser Pro	
410 415 420	
aat aaa gaa ctt att gca gtt gat aat gaa aac aac act ttg aaa gtt	1889
Asn Lys Glu Leu Ile Ala Val Asp Asn Glu Asn Asn Thr Leu Lys Val	
425 430 435	
tcg gga tta gat gta agt aac gat gtt tca gat ggc aac ttc tgg gct	1937

Ser Gly Leu Asp Val	Ser Asn Asp Val	Ser Asp Gly Asn Phe Trp Ala	
440	445	450	455
aat gct cgt ctt tct gcc aac ggt tgg gga aaa agt gtt gat att tta			1985
Asn Ala Arg Leu Ser Ala Asn Gly Trp Gly Lys Ser Val Asp Ile Leu			
460	465	470	
ggg gct gag aag ctt aca atg gat gtt att gtt gat gaa cca acg acg			2033
Gly Ala Glu Lys Leu Thr Met Asp Val Ile Val Asp Glu Pro Thr Thr			
475	480	485	
gta gct att gcg gcg att cca caa agt agt aaa agt gga tgg gca aat			2081
Val Ala Ile Ala Ala Ile Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn			
490	495	500	
cca gag cgt gct gtt cga gtg aac gcg gaa gat ttt gtc cag caa acg			2129
Pro Glu Arg Ala Val Arg Val Asn Ala Glu Asp Phe Val Gln Gln Thr			
505	510	515	
gac ggt aag tat aaa gct gga tta aca att aca gga gaa gat gct cct			2177
Asp Gly Lys Tyr Lys Ala Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro			
520	525	530	535
aac cta aaa aat atc gct ttt cat gaa gaa gat aac aat atg aac aac			2225
Asn Leu Lys Asn Ile Ala Phe His Glu Glu Asp Asn Asn Met Asn Asn			
540	545	550	
atc att ctg ttc gtg gga act gat gca gct gac gtt att tac tta gat			2273
Ile Ile Leu Phe Val Gly Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp			
555	560	565	
aac att aaa gta att gga aca gaa gtt gaa att cca gtt gtt cat gat			2321
Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile Pro Val Val His Asp			
570	575	580	
cca aaa gga gaa gct gtt ctt cct tct gtt ttt gaa gac ggt aca cgt			2369
Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe Glu Asp Gly Thr Arg			
585	590	595	
caa ggt tgg gac tgg gct gga gag tct ggt gtg aaa aca gct tta aca			2417
Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr			
600	605	610	615
att gaa gaa gca aac ggt tct aac gcg tta tca tgg gaa ttt gga tat			2465
Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr			
620	625	630	
cca gaa gta aaa cct agt gat aac tgg gca aca gct cca cgt tta gat			2513
Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp			
635	640	645	
ttc tgg aaa tct gac ttg gtt cgc ggt gag aat gat tat gta gct ttt			2561
Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn Asp Tyr Val Ala Phe			
650	655	660	
gat ttc tat cta gat cca gtt cgt gca aca gaa ggc gca atg aat atc			2609
Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile			

665	670	675	
aat tta gta ttc cag cca cct act aac ggg tat tgg gta caa gca cca			2657
Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro			
680	685	690	695
aaa acg tat acg att aac ttt gat gaa tta gag gaa gcg aat caa gta			2705
Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu Glu Ala Asn Gln Val			
700	705	710	
aat ggt tta tat cac tat gaa gtg aaa att aac gta aga gat att aca			2753
Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr			
715	720	725	
aac att caa gat gac acg tta cta cgt aac atg atg atc att ttt gca			2801
Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met Met Ile Ile Phe Ala			
730	735	740	
gat gta gaa agt gac ttt gca ggg aga gtc ttt gta gat aat gtt cgt			2849
Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg			
745	750	755	
ttt gag ggg gct gct act act gag ccg gtt gaa cca gag cca gtt gat			2897
Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp			
760	765	770	775
cct ggc gaa gag acg cca cct gtc gat gag aag gaa gcg aaa aaa gaa			2945
Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu			
780	785	790	
caa aaa gaa gca gag aaa gaa gag aaa gaa gca gta aaa gaa gaa aag			2993
Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys			
795	800	805	
aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa			3041
Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys			
810	815	820	
aaa taatctatta aactagttat agggttatct aaaggtctga tgtagatctt			3094
Lys			
ttagataacc tttttcttgc ataactggac acagagttgt tattaagaa agtaag			3150

<210> 2
 <211> 824
 <212> PRT
 <213> Bacillus sp. KSM-S237

 <400> 2

Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile Leu Ile			
1	5	10	15
Leu Val Leu Leu Leu Ser Leu Phe Pro Ala Ala Leu Ala Ala Glu Gly			

20

25

30

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
 35 40 45

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
 50 55 60

Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
 65 70 75 80

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
 85 90 95

Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu
 100 105 110

Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile
 115 120 125

Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met
 130 135 140

Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
 145 150 155 160

Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu
 165 170 175

Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser
 180 185 190

Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
 195 200 205

Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys
 210 215 220

Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
 225 230 235 240

Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
 245 250 255

Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
260 265 270

Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
275 280 285

Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
290 295 300

Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp
305 310 315 320

Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
325 330 335

Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
340 345 350

Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro
355 360 365

Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val
370 375 380

Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys
385 390 395 400

Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe
405 410 415

Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn
420 425 430

Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val
435 440 445

Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp
450 455 460

Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val
465 470 475 480

Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile Pro Gln Ser
485 490 495

Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg Val Asn Ala
500 505 510

Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr
515 520 525

Ile Thr Gly Glu Asp Ala Pro Asn Leu